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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                            Result
No.
 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
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1877
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Match Length DB
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O58106 pyrococcus
P74630 synechocyst
O97bm4 thermoplasm
O97gf3 clostridium
O973t0 sulfolobus
O973t0 sulfolobus
O973t0 sulfolobus
O970pp sulfolobus
 o50094 pyrococcus O9kd04 bacillus ha O9v294 pyrococcus O9h191 thermoplasm O30246 archaeoglob O9v0m7 pyrococcus O83377 treponema p O97zd2 sulfolobus O53278 mycobacteri
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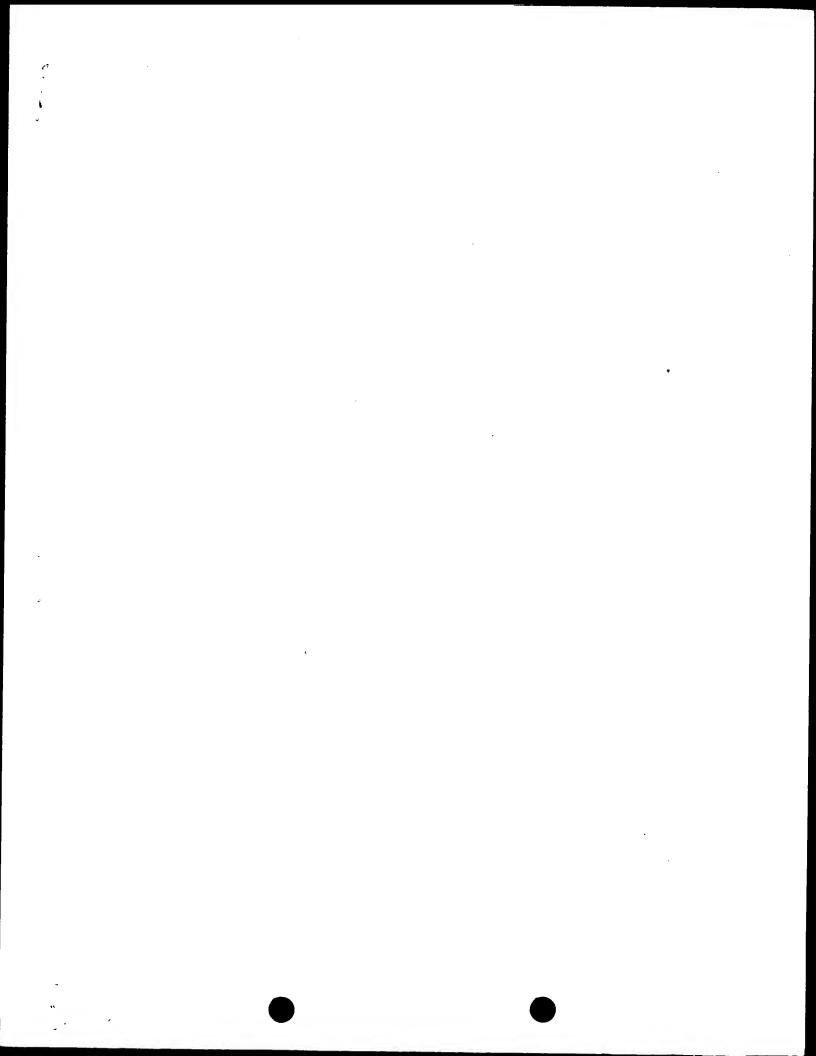
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Q9uyco pyrococcus	17 Q9UYC0	394	5.1	95	4
and a standard standa	2 Q9Z597	296	5.1	95	44
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specific process		1134	5.1	95.5	42
		1150	5.1	96	41
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		636	5.1	96	39
σ	13 Q918E8	197	5.1	96.5	38
Ω	5 Q9VR32	929	5.2	97	37
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α		531	5.2	97	35 5
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	16 Q97M42	266	5.4	100.5	23
	13 013132	754	5.4	102	22
	13 013131	754	5.5	103	21
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Tried opposed	10 Q9MBD0		5.5	103.5	19
Q9zvn2 arabidopsis			5.5	104	18
	17 Q97YY0	902	5.6	105.5	17

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RESULT

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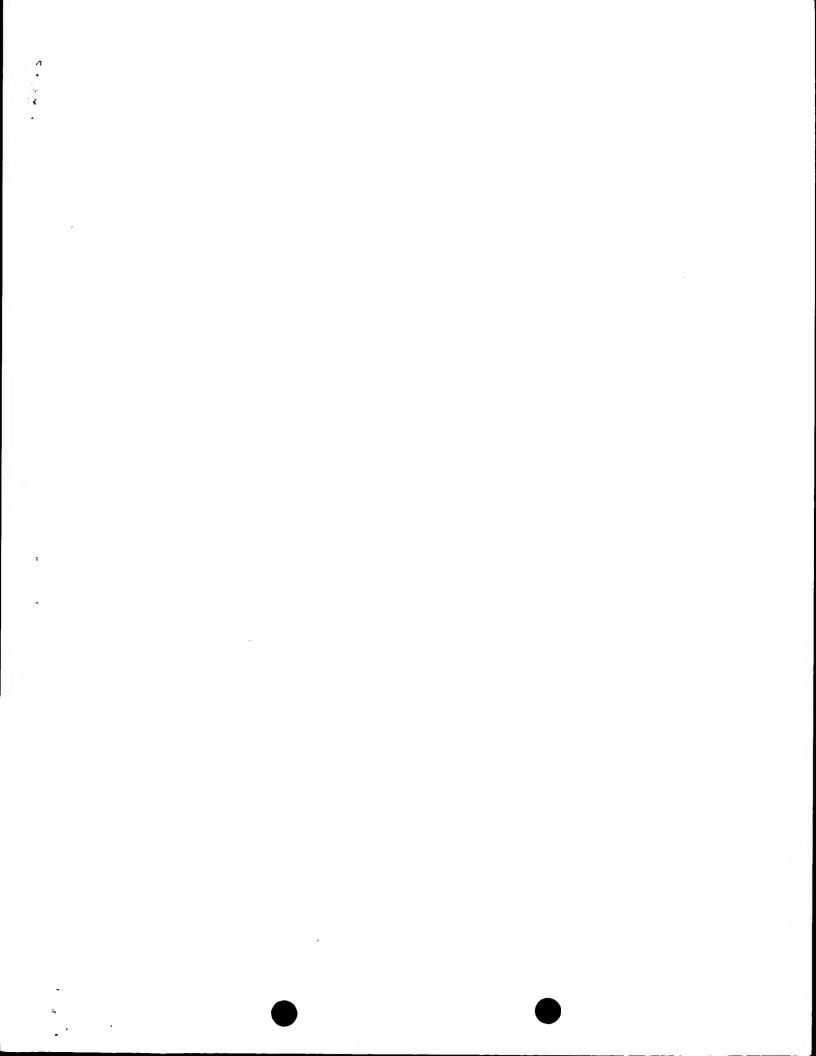
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Pr03065; Glycc_hydro_57; 1.
hetical protein; Complete prote
NCE 364 AA; 41755 MW; 7B4B3
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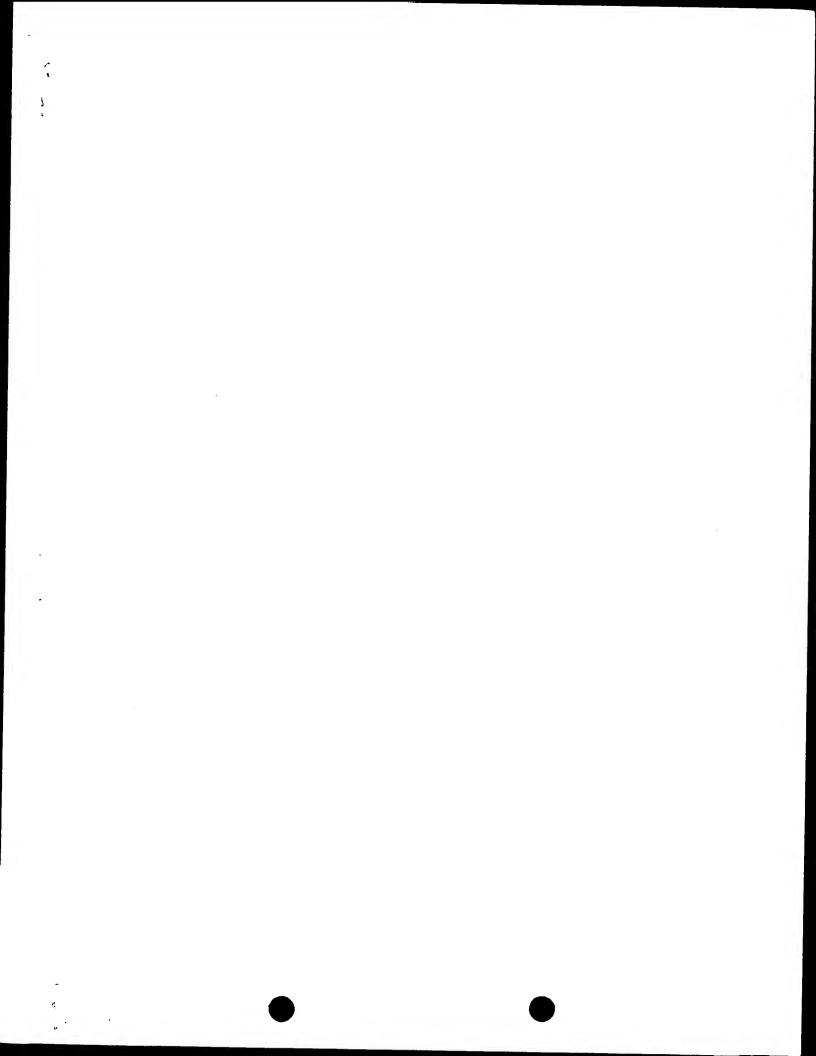
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Hypothetical protein; Complete
SEQUENCE 529 AA; 62075 MW;
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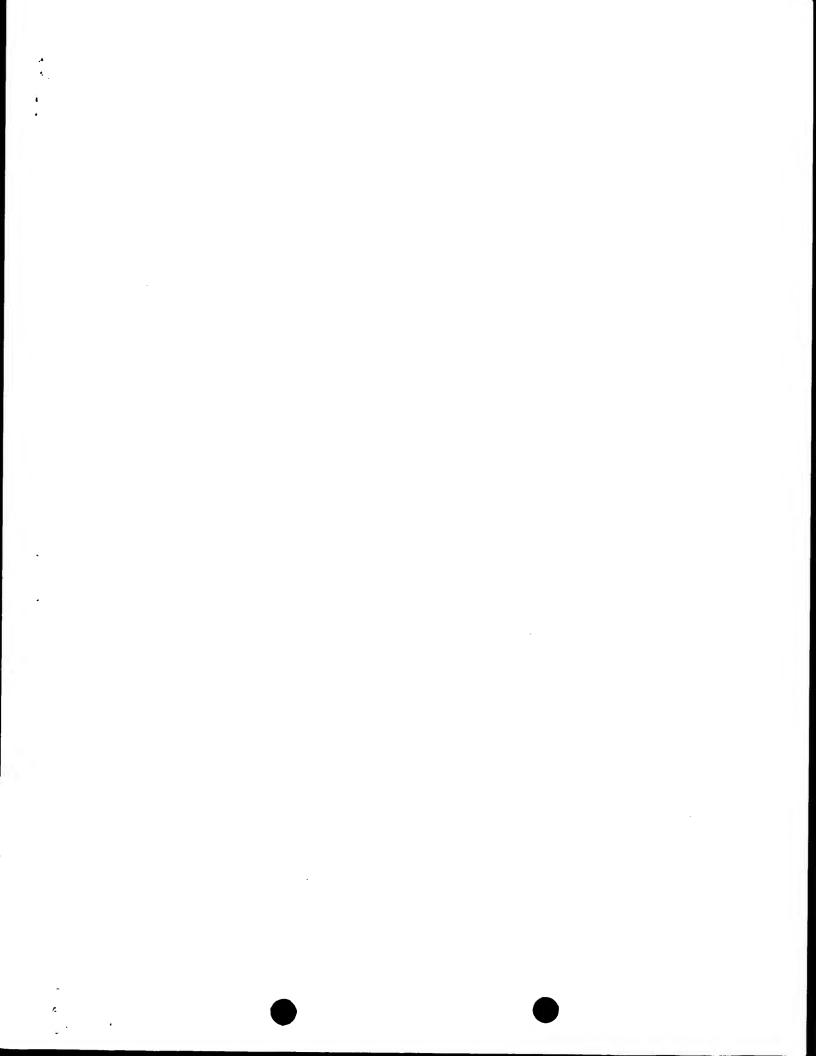


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Murphy,D. and Reid,J.
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179198. .221284
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70234. .106104
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42734. .70133
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28792. .42633
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11008. .14713
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1.8%; Score 20; DB 6; 100.0%; Pred. No. 16; tive 0; Mismatches
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92046037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-NOV-1990) M. Carrington, CARPARTMENT OF BIOCHEMISTRY, TENNIS COURT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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121. .159
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/db_xref="SWISS-PROT: P26329"
/translation="MVYRNILQLSVLKVLIYLIVEATHFGVKYELMOPECELTAELR
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DNIANGIDRAVRATAYASEAAGALFESIQTLHDATDGTTYCLSASGQGKNAASTTELL
GVQFSGGSRINLGLGAIVASSAAQQPTRPDLSDFSGTARNQADTLYGKAHASTTELL
GVQFSGGSRINLGLGAIVASSAAQQPTRPDLSDFSGTARNQADTLYGKAHASTTELL
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/protein_id="CAA40086.1"
/db_xref="GI:10454"
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1 389 c 389 g 316 t
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IAKLETEIADORGKSPEAECNKITEEPKCSEEKICSWHKEVKAGEKNCOFNSTKASKS
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/isolate="MIAG 209"
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RT ROAD, CAMBRIDGE CB2 1QW
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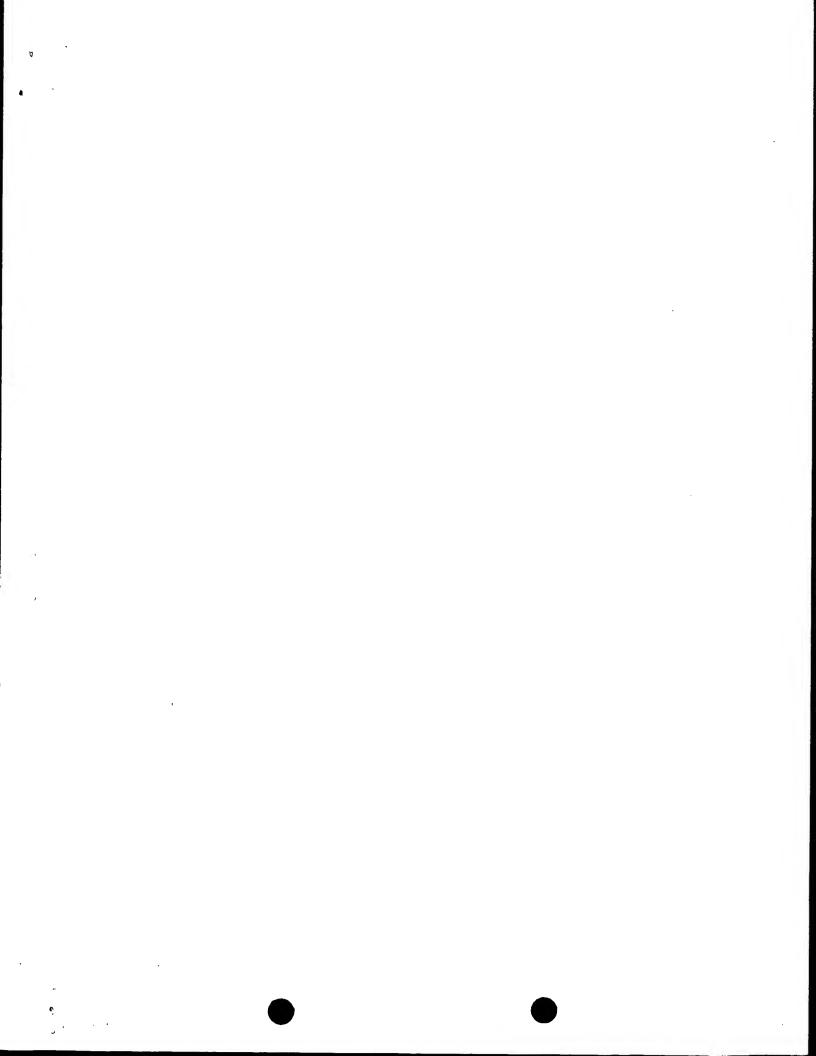
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \tt CTCAGGGAGCTTAGGAAGGCGATAAAGCTCGTTTTTGAAGGTAAGGTAACGCTAAAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACACCTTATAAAGGCCCAAAGGGAAAAGCGCTTTAGGTACATCAGCTATCTCCT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ccacaccttataaaggcccaaagggaaaagcgctttaggtacatcagctatctccttggt 540
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cccctccctgagaggaggctggatgccttccgggcgatatataacgattggaggggtgaa 1080
                                                                                                                                                                                                                                                                                                                                                                                                   aacattcttctatacggcaccgatatagagttcattggctatagggacattgcaggctac 780
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                                                                                                                                                                   gataagagcttgaggatatggagaggaggaaggaagggaacgcaagacttaatatgctgtcc 960
                                                                                                                                                                                                                                              ccctcagagctgaagcacagtggaagggagctctacttacggacttcgagttgggcacca 900
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                                                                                              tacaatatgaggggggaactcgcccttttagccgagaacagcgatgcaaggggatgggag 1020
                                                                                                                                                                                                                             CCCTCAGAGCTGAAGCACAGTGGAAGGGAGCTCTACTTACGGACTTCGAGTTGGG---
                                                                                                                                                                                                                                                                                                      AGAATGAGTGTTGAGGGATTATTAGAGGTTATAGACGAGCTCAACTCGGAACTGTGC
                                                                             TACAATATGAGGGGGGAACTCGCCTTTTTAGCCGAGAACAGCGATGCAAGGGGATG---G
                                                                                                                                                      GATAAGAGCTTGAGGATATGGAGAGAGGGACGAAGGGGAACGCAAGACTTAATATGCTG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus furiosus galactokinase (galK), alpha-galactosidase (galA), putative transporter (mfsA), beta-glucosidase (bglA), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF195244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-OCT-1999) Laboratory of Microbiology, Wageningen University and Research Center, Hesselink van Suchtelenweg 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.

1 (bases 1 to 5762)
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AP000002/c

DEFINITION Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position AP000002

257000 bp

DNA

linear

BCT 06-APR-2000

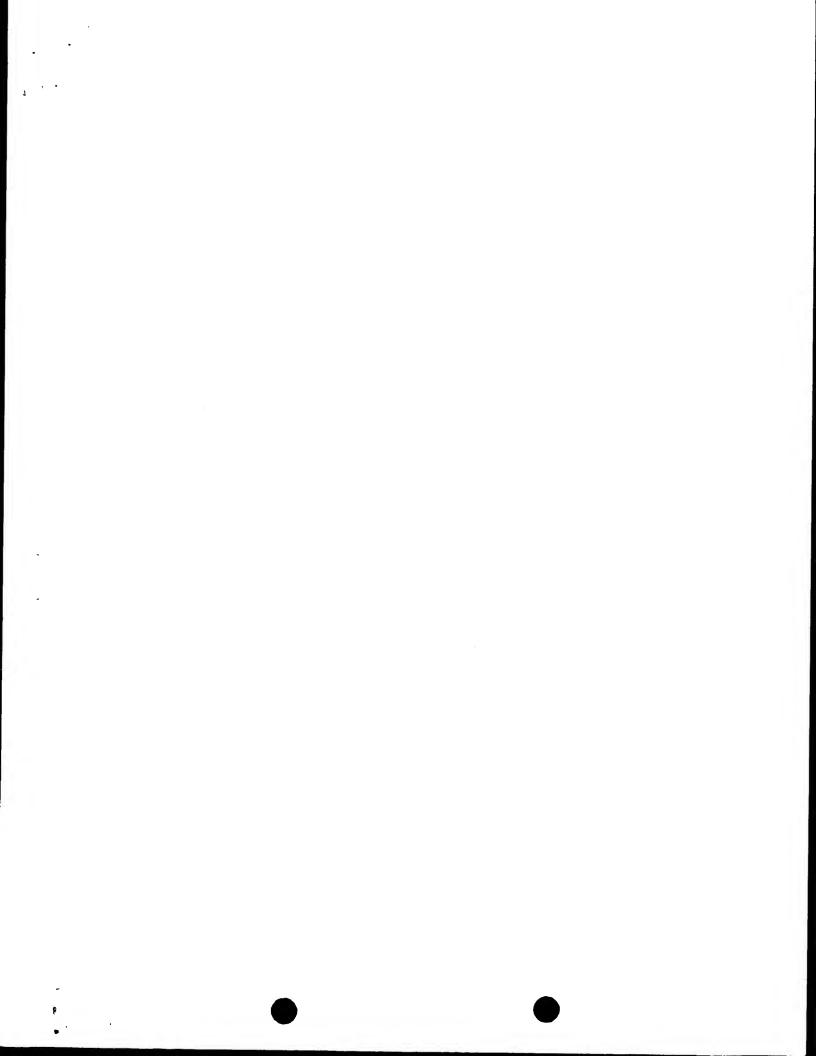
KEYWORDS ACCESSION

SOURCE ORGANISM REFERENCE

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AUTHORS AP000002 AB009475 AB009476 AB009477 AB009478 AB009479 AB009480 AB009481 AB009482 AB009483 AB009484 BA000001 AB000002.1 GI:3236129 Kawarabayasi,Y., Sawada,M., Horikawa,H., Yamamoto,S., Sekine,M., Baba,S., Kosugi,F Pyrococcus horikoshii (strain:OT3) DNA Pyrococcus horikoshii Thermococcaceae; Pyrococcus Archaea; Euryarchaeota; Thermococci; Thermococcales; (sites) Kosugi, H., Hosoyama, A., Nagai, Y., Haikawa,Y., Hino,Y.,



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (E-mail:genomeOTjenite.go.jp, Tel:+81-3-3481-8951, Fax:+81-3-3481-8424)
on Jul 28, 1998 this sequence version replaced gi:3130553 gi:31310577 gi:3130627 gi:3130656 gi:3130685 gi:3130705 gi:3130737 gi:3130785 gi:3130824 gi:3130828.
AB009475-AB009484: submitted (10-DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakai,M., Ogura,K., Otuka,R., Nakazawa,H., Takamiya,M., Ohfuku,Y., Funahahi,T., Tanaka,T., Kudoh,Y., Yamazaki,J., Kushida,N., Oguchi,A., Aoki,K., Nakamura,Y., Robb,T.F., Horikoshi,K., Makamura,Y., Robb,T.F., Horikoshi,K., Masuchi,Y., Shizuya,H. and Kikuchi,H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUN-1998) Yutaka Kawarabayasi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3 DNA Res. 5 (2), 55-76 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Restriction map, ORF organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center, URL: http://www.bio.nite.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 52.0; SwissProt release 34.0; PIR-Protein release 54.0; and OWL release 29.5. E-mail address for comments and questions: genomeOT3@nite.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maryland, Baltimore, MD, USA.
Horikoshi, K. is at the Japan Marine Science and Technology Center,
Yokosuka, Kanagawa 237-0061, Japan.
Masuchi, Y. is at the University of Tokyo, Meguro, Tokyo 153-0041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305-0046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawarabayasi, Y. is officially affiliated with the National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tanaka, T., Kawarabayasi, Y. and Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
All the sequence with length 100 codons or more between ATG or GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shizuya, H. is at the California Institute of Technology, Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute of Bioscience and Human-Technology, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The other authors are at the National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 257000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stop codon are defined as CDS
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GVEMFVKGDKVWANEVSPRPHDTGMVTLASHPPGFSEFALHLRAVLGLPIPGEWVDGY
                                                                                                                                                                                                                                                                   KDGY FVVPNARATWI AMHRERLRETLVKEAK VPTSRYMYATTLDELY EACEK IGY PCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="287001-544000 nt. position"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:53953"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism-"Pyrococcus horikoshii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .257000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             РН0318"
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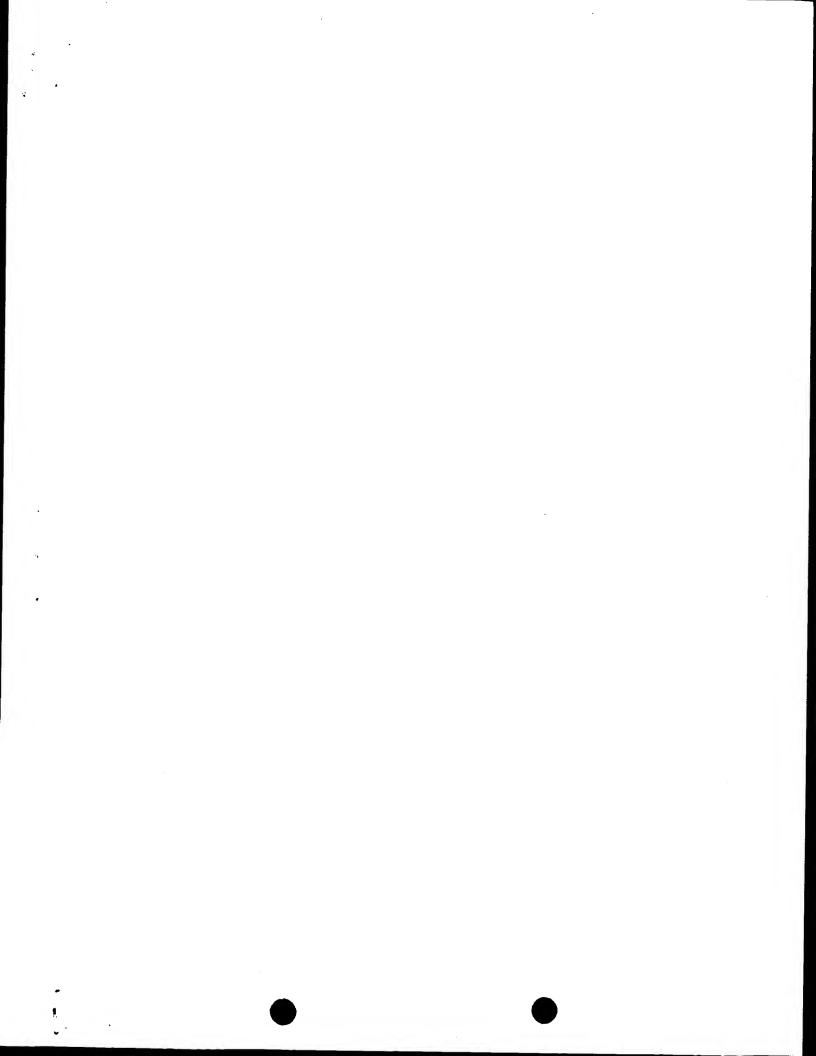
FEATURES

CDS

gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to ow1:SSOUREK percent identity: 68.000 in 150aa; PIR:S76001 percent identity: 60.694 in 173aa; ow1:BAPURKE1 percent identity: 62.329 in 146aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2653. .3186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2653. .3186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3275. .4036)
/gene="pH0321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAWITDLFTGLIEFIKGCSVHIPGSRNLCFLHKGFPKPLPVHSYPGSSCIWNYKITIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Translation="MISWEIBELDREIGKIKKHSLILIHEEDASSRGKDILFYILSRK
LKSDNLVGMFSISYPLQLIIRILSRFGVDVIKYLENHRLAIVDTFGSFHGIKATMPGV
WYLEGMLSSETLPIKYAKAVEDHKKVWMDLNLFEGRELYGFAISMSGYLEVFTPEETL
RYLETSAEVRYGHPAYKKYPRGTNFWLWEGVYDKRVLLSVYRRADYVLKTRSSLGENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="253aa long hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKAKRLEEMGWERYLSE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"GI:3256710"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4856. .6172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mgiieelvssipeggilaiiokelesegdregllvlkhllen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"PH0322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4039. .4698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKRELLVIKTPKPIEELVRFEYEFKGNEPKLRRVD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PH0321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDSLLSIVQMPSGIPVATVAIDNAKNAALLALRILGIKYPEIKEKLRRYMKDMKRKVE
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                                                                                                                                                                                                                                                                                                                                         motif-prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYRPKTIITYSQLECPILEETVYLASDIVLETRIINGKKVGIITKGPNENLIFELFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
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NKAWAREFMERNNIPGRKMFRIFDDVQEMRKWIDEYGKPVVVKPLGLTGGKGVKVVGY
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Matches
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                                                                                                                                                                                                                                       45405 CAATTCTTCCACTCCTCACCCTCTCCAGGATTGAGGCCCCAAATAAAACGTGATAGAGAGA 45346
                                                                                                                                                                                                                                                                                                                                                              45465
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45285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tgagagcgctcgtctttcacggcaacctccagtatgccgaaatcccaaagagcgaaatcc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cttttgggctcaacataacgggctataccttáaagttcctcccgaaggatattatagacc 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caaaggtcatagagaaggcatacatcccagtcatcgagacactgattaaagaagaaattc 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTCGGCCTAAACATAACCGGTTATTCACTGCAATTTCTCCCCCAGGAATTAATCCACC 45466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGGTTATAGAAAAATCCTACTTTCCAACTATTTCGGAGCTTATAAAAAGGGAGATAC 45526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGAGCATTGATCTTCCATGGAAATTTGCAATACGCCGAAATACCAAAGCATGAAATCT 45586
                                                                                                                                                ttaaggaagagctcttcgagctttctccaaagggattctggctgccagagctcgcctatg 361
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                                                                                                                                                                                                                                                                                                                                                                                              ATCCGATAATTCCAGCAATTTTAAGAGACAATGAATACGAATATCTCTTTGCCGACGGAG
                                                     acccgataatccctgccatactgaaggacaacggttatgagtatctattcgccgacgggg 421
                                                                                                                                                                                                                                                                                             caatactccccctcctcccgcttagcagagtagaagcacaagttcagagagatagggaag 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748;
                                                                                                                   TAAAGGAAGATATTCGAGGTTTCTCCTGGAGGATTTTGGCTTCCCGAGTTGGCCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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6174. .7325
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BILGAVTGLSAVYPNSPRLVGISGLLYGVAGALSMGIGALISVRSQROVSEAIRERTK
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/protein_id-"BAA29399.1"
/db_xref-"Gi:3256716"
/translation-"MSSAIKIAEEFYNDEYSDSVLYAELAKYEKNKEIKEEFLRLSRM
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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